

**FIGURE 1****Target segment starts with AA**

Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
AAGATCCTCAAGAATGACGCC [SEQ ID NO:18]	0.48	117	GAUCCUCAAGAAUGACGCCUU [SEQ ID NO:35] UUCUAGGAGUUCUUACUGCGG [SEQ ID NO:52]
AAGAATGACGCCTACCGCAAC [SEQ ID NO:19]	0.52	126	GAAUGACGCCUACCGCAACUU [SEQ ID NO:36] UUCUUACUGCGGAUGGCGUUG [SEQ ID NO:53]
AACCGCATCATCAAGAACGAG [SEQ ID NO:20]	0.48	144	CCGCAUCAUCAAGAACGAGUU [SEQ ID NO:37] UUGGCGUAGUAGUUCUUGCUC [SEQ ID NO:54]
AAGAACGAGCTGAAGCTGCTG [SEQ ID NO:21]	0.52	156	GAACGAGCUGAAGCUGCUGUU [SEQ ID NO:38] UUCUUGCUCGACUUCGACGAC [SEQ ID NO:55]
AAGGAGCTGGCTATCATCCAC [SEQ ID NO:22]	0.52	381	GGAGCUGGCUAUCAUCCACUU [SEQ ID NO:39] UUCCUCGACCGAUAGUAGGUG [SEQ ID NO:56]
AAGCCTGAGAACATCATGCTG [SEQ ID NO:23]	0.48	411	GCCUGAGAACAUAUGCUGUU [SEQ ID NO:40] UUCGGACUCUUGUAGUACGAC [SEQ ID NO:57]
AACATCATGCTGGTGGACCAG [SEQ ID NO:24]	0.52	420	CAUCAUGCUGGUGGACCAGUU [SEQ ID NO:41] UUGUAGUACGACCACCUGGUC [SEQ ID NO:58]
AAGGTGATTGACTTCGGATCC [SEQ ID NO:25]	0.48	462	GGUGAUUGACUUCGGAUCCUU [SEQ ID NO:42] UUCCACUACUGAAGCCUAGG [SEQ ID NO:59]
AAGGAGCCATACATCCAGTCG [SEQ ID NO:26]	0.52	513	GGAGCCAUACAUCAGUCGUU [SEQ ID NO:43] UUCCUCGGUAGUAGGUCAGC [SEQ ID NO:60]

AACAACGAGTACGACCAGGTG [SEQ ID NO:27]	0.52	651	CAACGAGUACGACCAGGUGUU [SEQ ID NO:44] UUGUUGCUC AUGCUGGUCCAC [SEQ ID NO:61]
AAGTCGTTGGACCAGATTGAG [SEQ ID NO:28]	0.48	855	GUCGUUGGACCAGAUUGAGUU [SEQ ID NO:45] UUCAGCAACCUGGUCU AACUC [SEQ ID NO:62]
AAGAGCATGGTGGAGCTGATC [SEQ ID NO:29]	0.52	951	GAGCAUGGUGGAGCUGAUCUU [SEQ ID NO:46] UUCUCGUACCACCUCGACUAG [SEQ ID NO:63]
AATGCGGTCTCCGACATGATG [SEQ ID NO:30]	0.52	1341	UGCGGUCUCCGACAUGAUGUU [SEQ ID NO:47] UUACGCCAGAGGCUGUACUAC [SEQ ID NO:64]
AAGTCCGACTCCAACTTCAGC [SEQ ID NO:31]	0.52	1485	GUCCGACUCCAACUUCAGCUU [SEQ ID NO:48] UUCAGGCUGAGGUUGAAGUCG [SEQ ID NO:65]
AACTTCAGCAACCTCATTCGG [SEQ ID NO:32]	0.48	1497	CUUCAGCAACCUCAUUCGGUU [SEQ ID NO:49] UUGAAGUCGUUGGAGUAAGCC [SEQ ID NO:66]
AACATGACCATGGAAGCTGAG [SEQ ID NO:33]	0.48	1647	CAUGACCAUGGAAGCUGAGUU [SEQ ID NO:50] UUGUACUGGUACCUUCGACUC [SEQ ID NO:67]
AATGGCTGAGTGAGCCAGACT [SEQ ID NO:34]	0.52	1711	UGGCUGAGUGAGCCAGACUUU [SEQ ID NO:51] UUACCGACUCACUCGGUCUGA [SEQ ID NO:68]

**Target segment starts with CA**

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
CAAGATCCTCAAGAATGACGC [SEQ ID NO:69]	0.48	116	AGAUCCUCAAGAAUGACGCUU [SEQ ID NO:89] UUUCUAGGAGUUCUACUGCG [SEQ ID NO:109]
CAAGAATGACGCCTACCGCAA [SEQ ID NO:70]	0.52	125	AGAAUGACGCCUACCGCAAUU [SEQ ID NO:90] UUUCUUACUGCGGAUGGCGUU [SEQ ID NO:110]

CAACCGCATCATCAAGAACGA [SEQ ID NO:71]	0.48	143	ACCGCAUCAUCAAGAACGAUU [SEQ ID NO:91] UUUGGCGUAGUAGUUCUUGCU [SEQ ID NO:111]
CATCAAGAACGAGCTGAAGCT [SEQ ID NO:72]	0.48	152	UCAAGAACGAGCUGAAGCUUU [SEQ ID NO:92] UUAGUUCUUGCUCGACUUCGA [SEQ ID NO:112]
CAAGAACGAGCTGAAGCTGCT [SEQ ID NO:73]	0.52	155	AGAACGAGCUGAAGCUGCUUU [SEQ ID NO:93] UUUCUUGCUCGACUUCGACGA [SEQ ID NO:113]
CATCCGCTTCCTTGAGTTCTT [SEQ ID NO:74]	0.48	215	UCCGCUUCCUUGAGUUCUUUU [SEQ ID NO:94] UUAGGCGAAGGAACUCAAGAA [SEQ ID NO:114]
CAGAAGGAGAACAACCTTCGCG [SEQ ID NO:75]	0.52	297	GAAGGAGAACAACUUCGCGUU [SEQ ID NO:95] UUCUCCUCUUGUUGAAGCGC [SEQ ID NO:115]
CAAGGAGCTGGCTATCATCCA [SEQ ID NO:76]	0.52	380	AGGAGCUGGCUAUCAUCCAUU [SEQ ID NO:96] UUUCCUCGACCGAUAGUAGGU [SEQ ID NO:116]
CAAGCCTGAGAACATCATGCT [SEQ ID NO:77]	0.48	410	AGCCUGAGAACAUCAUGCUUU [SEQ ID NO:97] UUUCGGACUCUUGUAGUACGA [SEQ ID NO:117]
CAAGGTGATTGACTTCGGATC [SEQ ID NO:78]	0.48	461	AGGUGAUUGACUUCGGAUCUU [SEQ ID NO:98] UUUCCACUAACUGAAGCCUAG [SEQ ID NO:118]
CATACATCCAGTCGCGCTTCT [SEQ ID NO:79]	0.52	520	UACAUCCAGUCGCGCUUCUUU [SEQ ID NO:99] UUAUGUAGGUCAGCGCGAAGA [SEQ ID NO:119]
CAACAACGAGTACGACCAGGT [SEQ ID NO:80]	0.52	650	ACAACGAGUACGACCAGGUUU [SEQ ID NO:100] UUUGUUGCUCUUGCUGGUCCA [SEQ ID NO:120]
CACCACTTCTTCAAGCGCAAC [SEQ ID NO:81]	0.52	735	CCACUUCUUAAGCGCAACUU [SEQ ID NO:101] UUGGUGAAGAAGUUCGCGUUG [SEQ ID NO:121]

CAAGTCGTTGGACCAGATTGA [SEQ ID NO:82]	0.48	854	AGUCGUUGGACCAGAUUGAUU [SEQ ID NO:102] UUUCAGCAACCUUGGUCUAACU [SEQ ID NO:122]
CAAGAGCATGGTGGAGCTGAT [SEQ ID NO:83]	0.52	950	AGAGCAUGGUGGAGCUGAUUU [SEQ ID NO:103] UUUCUCGUACCACCUCGACUA [SEQ ID NO:123]
CAATGCGGTCTCCGACATGAT [SEQ ID NO:84]	0.52	1340	AUGCGGUCUCCGACAUGAUUU [SEQ ID NO:104] UUUACGCCAGAGGCUGUACUA [SEQ ID NO:124]
CAAGTCCGACTCCAACCTCAG [SEQ ID NO:85]	0.52	1484	AGUCCGACUCCAACUUCAGUU [SEQ ID NO:105] UUUCAGGCUGAGGUUGAAGUC [SEQ ID NO:125]
CAACTTCAGCAACCTCATTCG [SEQ ID NO:86]	0.48	1496	ACUUCAGCAACCUCAUUCGUU [SEQ ID NO:106] UUUGAAGUCGUUGGAGUAAGC [SEQ ID NO:126]
CAACATGACCATGGAAGCTGA [SEQ ID NO:87]	0.48	1646	ACAUGACCAUGGAAGCUGAUU [SEQ ID NO:107] UUUGUACUGGUACCUUCGACU [SEQ ID NO:127]
CATGACCATGGAAGCTGAGAG [SEQ ID NO:88]	0.52	1649	UGACCAUGGAAGCUGAGAGUU [SEQ ID NO:108] UUACUGGUACCUUCGACUCUC [SEQ ID NO:128]

**Target segment starts with GA**

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
GAGATGGTGGCCATCAAGATC [SEQ ID NO:129]	0.52	102	GAUGGUGGCCAUCAAGAUCUU [SEQ ID NO:144] UUCUACCACCGGUAGUUCUAG [SEQ ID NO:159]
GATGGTGGCCATCAAGATCCT [SEQ ID NO:130]	0.52	104	UGGUGGCCAUCAAGAUCUUU [SEQ ID NO:145] UUACCACCGGUAGUUCUAGGA [SEQ ID NO:160]
GATCCTCAAGAATGACGCCTA [SEQ ID NO:131]	0.48	119	UCCUCAAGAAUGACGCCUAUU [SEQ ID NO:146] UUAGGAGUUCUUACUGCGGAU [SEQ ID NO:161]

GAGTTCCAGAAGGAGAACAAC [SEQ ID NO:132]	0.48	291	GUUCCAGAAGGAGAACAACUU [SEQ ID NO:147] UUCAAGGUCUCCUCUUGUUG [SEQ ID NO:162]
GATCTCAAGCCTGAGAACATC [SEQ ID NO:133]	0.48	405	UCUCAAGCCUGAGAACAUCUU [SEQ ID NO:148] UUAGAGUUCGGACUCUUGUAG [SEQ ID NO:163]
GAGAACATCATGCTGGTGGAC [SEQ ID NO:134]	0.52	417	GAACAUCAUGCUGGUGGACUU [SEQ ID NO:149] UUCUUGUAGUACGACCACCUG [SEQ ID NO:164]
GAACATCATGCTGGTGGACCA [SEQ ID NO:135]	0.52	419	ACAUCAUGCUGGUGGACCAUU [SEQ ID NO:150] UUUGUAGUACGACCACCUGGU [SEQ ID NO:165]
GAAGGAGCCATACATCCAGTC [SEQ ID NO:136]	0.52	512	AGGAGCCAUACAUCAGUCUU [SEQ ID NO:151] UUUCCUCGGUAUGUAGGUCAG [SEQ ID NO:166]
GATTGAGACAGTGAATGGTGG [SEQ ID NO:137]	0.48	869	UUGAGACAGUGAAUGGUGGUU [SEQ ID NO:152] UUAACUCUGUCACUUACCACC [SEQ ID NO:167]
GAGACAGTGAATGGTGGCAGT [SEQ ID NO:138]	0.52	873	GACAGUGAAUGGUGGCAGUUU [SEQ ID NO:153] UUCUGUCACUUACCACCGUCA [SEQ ID NO:168]
GACAGTGAATGGTGGCAGTGT [SEQ ID NO:139]	0.52	875	CAGUGAAUGGUGGCAGUGUUU [SEQ ID NO:154] UUGUCACUUACCACCGUCACA [SEQ ID NO:169]
GAGCATGGTGGAGCTGATCAA [SEQ ID NO:140]	0.52	953	GCAUGGUGGAGCUGAUCAAUU [SEQ ID NO:155] UUCGUACCACCUCGACUAGUU [SEQ ID NO:170]
GAGAAGGCACCAGGTATGCAA [SEQ ID NO:141]	0.52	1248	GAAGGCACCAGGUAUGCAAUU [SEQ ID NO:156] UUCUCCGUGGUCCAUACGUU [SEQ ID NO:171]
GACTCCAACCTTCAGCAACCTC [SEQ ID NO:142]	0.52	1491	CUCCAACUUCAGCAACCUCUU [SEQ ID NO:157] UUGAGGUUGAAGUCGUUGGAG [SEQ ID NO:172]

GACAACATGACCATGGAAGCT [SEQ ID NO:143]	0.48	1644	CAACAUGACCAUGGAAGCUUU [SEQ ID NO:158] UUGUUGUACUGGUACCUUCGA [SEQ ID NO:173]
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**Target segment starts with TA**

Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
TACCGCAACCGCATCATCAAG [SEQ ID NO:174]	0.52	138	CCGCAACCGCAUCAUCAAGUU [SEQ ID NO:180] UUGGCGUUGGCGUAGUAGUUC [SEQ ID NO:186]
TACGTGAAGGAGCCATACATC [SEQ ID NO:175]	0.48	507	CGUGAAGGAGCCAUACAUCUU [SEQ ID NO:181] UUGCACUCCUCGGUAUGUAG [SEQ ID NO:187]
TACATCCAGTCGCGCTTCTAC [SEQ ID NO:176]	0.52	522	CAUCCAGUCGCGCUUCUACUU [SEQ ID NO:182] UUGUAGGUCAGCGCAAGAUG [SEQ ID NO:188]
TATGCTCAAGTCGTTGGACCA [SEQ ID NO:177]	0.48	848	UGCUC AAGUCGUUGGACCAUU [SEQ ID NO:183] UUACGAGUUCAGCAACCUGGU [SEQ ID NO:189]
TACTACTGTCTGGCTGAGGAG [SEQ ID NO:178]	0.52	1173	CUACUGUCUGGCUGAGGAGUU [SEQ ID NO:184] UUGAUGACAGACCGACUCCUC [SEQ ID NO:190]
TACTGTCTGGCTGAGGAGAAG [SEQ ID NO:179]	0.52	1176	CUGUCUGGCUGAGGAGAAGUU [SEQ ID NO:185] UUGACAGACCGACUCCUCUUC [SEQ ID NO:191]

## FIGURE 2

### A

#### Protein Sequence of Human HIPK4

Total length -- 616 AA

MSTIQSETDCYDIIIEVLGKGTGFEVAKGWRRSTGEMVAIKILKNDAYRNRIKKNELKLLHCMRGLDPEEAHVIRFLEFFH  
DALKFYLVFELLEQNLFQKNNFAPLPAHIRTVTLQVLTALARLKEIAIHADLKPENIMLVDQTRCPFRVKVIDFG  
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH  
AACKAHFFFKRNPHPDANPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSSVASRLTFPDREALAEHADLKSM  
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHETTHYYQLSLRSYRLSLQVEGKPPTPVVAAEDGTPYYCLAEKE  
AAGMGSVAGSSPFFREEKAPGMQRAIDQLDDLSLQEAGHGLWGETCTNAVSDMMVPLKAAITGHHVPDSGPEPILAFYSS  
RLAGRHKARKPPAGSKSDSNFSNLIRLSQVSPEDDRPCRGSSWEEGHLGASAEPLAILQRDEDGPNIDNMTMEAERPDP  
ELFDPSSCPGEWLSEPDCTLESVRGPRAQGLPPRRSHQHGPFRGATSFLQHVTGHH

### B

#### ATP Binding Domain -- 17-40 (predicted)

LGKGTGFEVAKGWRRSTGEMVAIK

### C

#### Serine/Threonine Binding Domain -- 132-144 (predicted)

IIHADLKPENIML

### D

#### Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTGFEVAKGWRRSTGEMVAIKILKNDAYRNRIKKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFE  
LLEQNLFQKNNFAPLPAHIRTVTLQVLTALARLKEIAIHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY  
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAACKAHFFK  
RNPHPDANPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSSVASRLTFPDREALAEHADLKSMVELIKRMLTW  
ESHERISPSAALRHPFV

### FIGURE 3

#### A

##### Protein Sequence of Mouse HIPK4

Total length -- 616 AA

MATIQSETDCYDIIIEVLGKGTFGGEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFH  
DALKFYLVFELLEQNLFQKNNFAPLPARHIRTVTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFG  
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH  
AARKAHFFKRNPHPDATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSM  
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHEATRYYQLSLRGCRLSLQVDGKPPPPVIAAEDGPPYYRLAEEE  
ETAGLGGVTGSGSFFREDKAPGMQRAIDQLDDLSLQEARRGLWS DTRADMVSDMLVPLKVASTSHRVPDSGPEPILAFYG  
SRLTGHRHKARKAPAGSKSDSNFSNLIRLSQASPEDAGPCRGSGWEEGEGRTTSTEPSVIPQREGDGPGIKDRPMDAERPG  
PELFDPPSSCPGEWLSEPEWTLLEGIRGSRAQGLPAHHPHPHGPPRTTSFLQHVGGHH

#### B

##### ATP Binding Domain -- 17-40 (predicted)

LGKGTFGGEVAKGWRRSTGEMVAIK

#### C

##### Serine/Threonine Binding Domain -- 132-144 (predicted)

IIHADLKPENIML

#### D

##### Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTFGGEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE  
LLEQNLFQKNNFAPLPARHIRTVTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY  
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHFFK  
RNPHPDATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSMVELIKRMLTW  
ESHERISPSAALRHPFV

## FIGURE 4

### A

#### Protein Sequence of Monkey HIPK4

Total length -- 616 AA

MATTQSETDCYDIIIEVLGKGTfGEVAKGWRRTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFH  
DALKFYLVFELLEQNLFQKNNFAPLPARHIRTVTLQVLRALARLKLAI IHADLKPENIMLVDQTRCPFRVKVIDFG  
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMaelHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH  
AARKAHFFKRNPHPDaanPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSVASRLTFPDREALAEHADLKSM  
VELIKRMLTWESHERISPSAALRHPFVSMQQLRNAHETTHYYQLSLRSYRLSLQVEGKPPAPVVAEDGTPYYRLAEEKE  
AAGMGSVASSSPFFREEKAPGMQRAIDQLDDLSLQEAGHGLWGETCTDVVSDMMAPLKAaitGRHMPDSGPEPILAFYSS  
RLAGRHKARKPPAGSKSDSNLSNLI RLSQVSPEDDRPCRGSSWEEGEHLGASAEPPAILQRDGDGPNIDNMTMEAERPDP  
ELFDPSSCPGEWLSEPdwTLEGVRGPRAQGLPpRRSHQHGPpRGATSFLLQHVtGHH

### B

#### ATP Binding Domain -- 17-40 (predicted)

LGKGTfGEVAKGWRRTGEMVAIK

### C

#### Serine/Threonine Binding Domain -- 132-144 (predicted)

IIHADLKPENIML

### D

#### Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTfGEVAKGWRRTGEMVAIKILKNDAYRNRIIKNELKLLHCMRGLDPEEAHVIRFLEFFHDALKFYLVFE  
LLEQNLFQKNNFAPLPARHIRTVTLQVLRALARLKLAI IHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY  
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMaelHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARKAHFFK  
RNPHPDaanPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGSVASRLTFPDREALAEHADLKSMVELIKRMLTW  
ESHERISPSAALRHPFV

## FIGURE 5

### A

#### Protein Sequence of Rat HIPK4

Total length -- 616 AA

MATIQSETDCYDIIIEVLGKGTFGGEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFH  
DALKFYLVFELLEQNLFQKNNFAPLPARHIRTVTTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFG  
SASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLH  
AARCAHFFKRNPHPDATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSM  
VELIKRMLTWESHERISPSAALRHPFVSMQQLRSAHEATRYQSLRGCRLSLQVDGKPPPPVIAAEDGPPYYRLAEEE  
ETAGLGGVTGSGSFFREDKAPGMQRAIDQLDDLSLQEARRGLWSDTRADMVSDMLVPLKVA STSHRVPDSGPEPILAFYG  
SRLTGRHKARKAPAGSKSDSNFSNLIRLSQASPEDAGPCRGSGWEEGEGRTTSTEPSVIPQREGDGPGIKDRPMDAERPG  
PELFDPPSSCPGEWLSEPEWTLEGI RGSRAQGLPAHHPHPHGPPRTTSFLQHVGGHH

### B

#### ATP Binding Domain -- 17-40 (predicted)

LGKGTFGGEVAKGWRRSTGEMVAIK

### C

#### Serine/Threonine Binding Domain -- 132-144 (predicted)

I IHADLKPENIML

### D

#### Protein Kinase Domain -- 11-347 (predicted)

YDIIIEVLGKGTFGGEVAKGWRRSTGEMVAIKILKNDAYRSRI IKNELKLLRCVRGLDPDEAHVIRFLEFFHDALKFYLVFE  
LLEQNLFQKNNFAPLPARHIRTVTTLQVLRALARLKE LAI IHADLKPENIMLVDQTRCPFRVKVIDFGSASIFSEVRY  
VKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCVMAELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAARCAHFFK  
RNPHPDATNPWQLKSSADYLAETKVRPLERRKYMLKSLDQIETVNGGGAVSRLSFPDREALAEHADLKSMVELIKRMLTW  
ESHERISPSAALRHPFV

## FIGURE 6

**A**

CLUSTAL W multiple sequence alignment results

MSF: 346 Type: P Check: 4900 ..

Name: mushipk3\_np\_034564.kd.pep oo Len: 346 Check: 9189 Weight: 7.5  
 Name: rathipk3\_np\_113975.kd.fas.pep oo Len: 346 Check: 347 Weight: 6.5  
 Name: humhipk3\_np\_005725.kd.pep oo Len: 346 Check: 9094 Weight: 7.8  
 Name: humhipk1-like\_ax318266.kd.pep oo Len: 346 Check: 773 Weight: 6.8  
 Name: mushipk1\_np\_034562.kd.pep oo Len: 346 Check: 878 Weight: 7.0  
 Name: humhipk2\_np\_073577.kd.fas.pep oo Len: 346 Check: 11 Weight: 6.7  
 Name: mushipk2\_np\_034563.kd.pep oo Len: 346 Check: 1047 Weight: 7.7  
 Name: wormf20b6\_q19632.kd.pep oo Len: 346 Check: 9639 Weight: 16.4  
 Name: humhipk4.kd.fas.pep oo Len: 346 Check: 4355 Weight: 5.4  
 Name: monkeyhipk4\_ab074449.kd.fas.pe oo Len: 346 Check: 4346 Weight: 5.3  
 Name: mushipk4.kd.fas.pep oo Len: 346 Check: 5897 Weight: 5.4  
 Name: rathipk4\_xp\_218355.kd.fas.pep oo Len: 346 Check: 5822 Weight: 4.8  
 Name: yeastyak1\_np\_012394.kd.fas.pep oo Len: 346 Check: 3415 Weight: 12.2  
 Name: dmcg17090\_q95tg3.kd.pep oo Len: 346 Check: 87 Weight: 26.0

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      1                                     50
mushipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
rathipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk3_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk1-lik YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
mushipk1_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk2_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
mushipk2_np_ YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
wormf20b6_q1 YEVLDFLGRG TFGQVVKCWK RGTNEIVAIAK ILKNHPSYAR QGQIEVSILA
humhipk4.kd. YDIEVLGK GTFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
monkeyhipk4_ YDIEVLGK GTFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
mushipk4.kd. YDIEVLGK GTFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
rathipk4_xp_ YDIEVLGK GTFGEVAKGWR RSTGEMVAIAK ILKNHPSYAR QGQIEVSILA
yeastyak1_np YLVDILGQG TFGQVVKCQN LLTKEILAVK VVKSRTYILT QSITEAKILE
dmcg17090_q9 ...YIFNCLD DIGQVNVPTD LEGGQLLAEK TDRREFIDLL KRMLTIDQER
  
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      51                                     100
mushipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
rathipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk3_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk1-lik RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
mushipk1_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk2_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
mushipk2_np_ RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
wormf20b6_q1 RLSTENA..D EYNFVRAYEC FQHRNHTCLV FEMLEQNLYD FLKQNKFSPL
humhipk4.kd. CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF EFKENNFAPL
monkeyhipk4_ CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF EFKENNFAPL
mushipk4.kd. CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF EFKENNFAPL
rathipk4_xp_ CMRGLDP..E EAHVIRFLEF FHDALKFYLV FELLEQNLF EFKENNFAPL
yeastyak1_np LLNQKIDPTN KHHFLRMYDS FVHKHNLCLV FELLSSNNLYE LLKQNKFHGL
dmcg17090_q9 RLTPAEALNH SFTRLTHLVD YVYCINNPKAS VQMMEVCRRG DFHTVQVQAST
  
```

	101				150
mushipk3_np_	PLKVIRPVLO	QVATALKKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID
rathipk3_np_	PLKVIRPVLO	QVATALKKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID
humhipk3_np_	PLKVIRPILQ	QVATALKKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID
humhipk1-lik	PLKYIRPILQ	QVATALMKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVFD
mushipk1_np_	PLKYIRPILQ	QVATALMKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID
humhipk2_np_	PLKYIRPVLO	QVATALMKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID
mushipk2_np_	PLKYIRPVLO	QVATALMKLK	SLGLIHADLK	PENIMLVDPV	RQPYRVKVID
wormf20b6_q1	PLNAIRPILF	QVLTALLKLK	SLGLIHADLK	PENIMLVDPQ	QPYRVKVID
humhipk4.kd.	PARHIRTVTL	QVLTALARLK	ELAIHADLK	PENIMLVDPQ	RCPFRVKVID
monkeyhipk4_	PARHIRTVTL	QVLRALARLK	ELAIHADLK	PENIMLVDPQ	RCPFRVKVID
mushipk4.kd.	PARHIRTVTL	QVLRALARLK	ELAIHADLK	PENIMLVDPQ	RCPFRVKVID
rathipk4_xp_	PARHIRTVTL	QVLRALARLK	ELAIHADLK	PENIMLVDPQ	RCPFRVKVID
yeastyak1_np	SIQLIRFTT	QILDCLVCLK	ESKLHCDLK	PENILLCAPD	KP..ELKIID
dmcg17090_q9	LVTNFVPSST	ENMTFTINNQ	LTSQVQRLVR	DGRPLAYEGL	YQIYNGRSVA

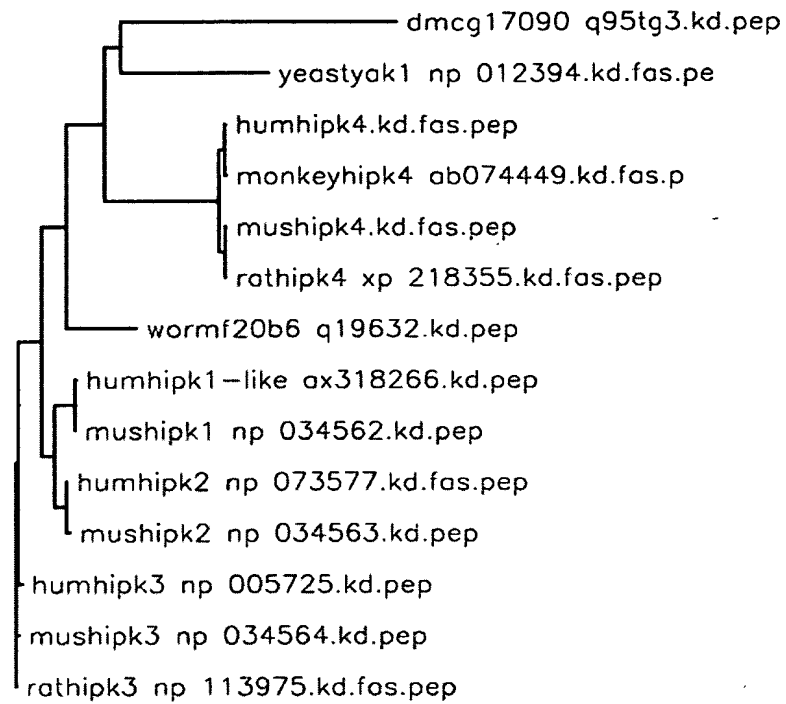
	151				200
mushipk3_np_	FGSASHVSKT	..VCSTYLQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL
rathipk3_np_	FGSASHVSKT	..VCSTYLQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL
humhipk3_np_	FGSASHVSKT	..VCSTYLQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL
humhipk1-lik	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL
mushipk1_np_	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL
humhipk2_np_	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL
mushipk2_np_	FGSASHVSKA	..VCSTYLQS	RYYRAPEIIL	GLPFCEAIDM	WSLGCVIAEL
wormf20b6_q1	FGSASHRSKA	..VTNTYLQS	RYYRAPEIIL	GLPFNCSIDM	WSLGCVIAEL
humhipk4.kd.	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPFCEKVDV	WSLGCVMAEL
monkeyhipk4_	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPFCEKVDV	WSLGCVMAEL
mushipk4.kd.	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPFCEKVDV	WSLGCVMAEL
rathipk4_xp_	FGSASIFSEV	RYVKEPYIQS	RFYRAPEILL	GLPFCEKVDV	WSLGCVMAEL
yeastyak1_np	FGSSCEEART	...VYTYIQS	RFYRAPEIIL	GIPYSTSIDM	WSLGCVIAEL
dmcg17090_q9	RQYP.....	...QTRTDS	FQHQLVSNIL	CPPSYQTMPS	PTKHVVVGS

	201				250
mushipk3_np_	FLGWPLYPGA	LEHDQIRYIS	QTQGLPGEQL	LNVGTKSTRF	FCRE.....
rathipk3_np_	FLGWPLYPGA	LEYDQIRYIS	QTQGLPGEQL	LNVGTKSTRF	FCRE.....
humhipk3_np_	FLGWPLYPGA	LEYDQIRYIS	QTQGLPGEQL	LNVGTKSTRF	FCRE.....
humhipk1-lik	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....
mushipk1_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....
humhipk2_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....
mushipk2_np_	FLGWPLYPGA	SEYDQIRYIS	QTQGLPAEYL	LSAGTKTTRF	FNRD.....
wormf20b6_q1	FLGWPLYPGS	SEYDQIRFII	QTQGLPPTSM	LESASKLHRF	FKEVKSESPN
humhipk4.kd.	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAACKAHHF	FKRNP.....
monkeyhipk4_	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAACKAHHF	FKRNP.....
mushipk4.kd.	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAACKAHHF	FKRNP.....
rathipk4_xp_	HLGWPLYPGN	NEYDQVRYIC	ETQGLPKPHL	LHAACKAHHF	FKRNP.....
yeastyak1_np	FLGIPIFPGA	SEYNQLTRII	DTLGYPSSWM	IDMGKNSGKF	MKKLAPEE..
dmcg17090_q9	TMQPPLQVPP	QQYVNVPPVP	SMVEPTSGQR	MLLTNRVQAS	GVAWPQTG..

	251				300
mushipk3_np_	.TDMSHSGWR	LKTLEEHEAE	TG.MKSKEAR	KYIFNSLDDI	VHVN.....T
rathipk3_np_	.TDMSHSGWR	LKTLEEHEAE	TG.MKSKEAR	KYIFNSLDDI	VHVN.....T
humhipk3_np_	.TDMSHSGWR	LKTLEEHEAE	TG.MKSKEAR	KYIFNSLDDV	AHVN.....T
humhipk1-lik	.PNLGYPLWR	LKTPEEHELE	TG.IKSKEAR	KYIFNCLDDM	AQVN.....M
mushipk1_np_	.PNLGYPLWR	LKTPEEHELE	TG.IKSKEAR	KYIFNCLDDM	AQVN.....M
humhipk2_np_	.TDSPLYLWR	LKTPDDHEAE	TG.IKSKEAR	KYIFNCLDDM	AQVN.....M
mushipk2_np_	.TDSPLYLWR	LKTPDDHEAE	TG.TKSKEAR	KYIFNCLDDM	AQGN.....M
wormf20b6_q1	HTNVGGSYR	LKTVEEYEAS	SSTAKSKETR	KYIFNVIDDI	SRVC.....Y
humhipk4.kd.	.HPDAANPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGSVAS
monkeyhipk4_	.HPDAANPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGSVAS
mushipk4.kd.	.HPDATNPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGGAVS
rathipk4_xp_	.HPDATNPWQ	LKSSADYLAE	TK.VRPLERR	KYMLKSLDQI	ETVNGGGAVN
yeastyak1_np	.SSSSTQKHR	MKTIEEFCRE	YNIVEKPSKQ	YFKWRKLPDI	IRNYR..YPK
dmcg17090_q9	RQMALVPSWP	QQAPAHSLIV	DSTPLFNVEE	IYPKHHLNLP	RNDLKKESPA

	301				346
mushipk3_np_	VMDLEGGDLL	AEKADRREFV	NLLKKMLLID	ADLRITPIET	LNHPFV
rathipk3_np_	VMDLEGSDLL	AEKADRREFV	SLLKKMLLID	ADLRITPIET	LNHPFV
humhipk3_np_	VMDLEGSDLL	AEKADRREFV	SLLKKMLLID	ADLRITPAET	LNHPFV
humhipk1-lik	STDLEGTDM	AEKADRREYI	DLLKKMLTID	ADKRITPLKT	LNHQFV
mushipk1_np_	STDLEGTDM	AEKADRREYI	DLLKKMLTID	ADKRITPLKT	LNHQFV
humhipk2_np_	TTDLEGSDML	VEKADRREFI	DLLKKMLTID	ADKRITPIET	LNHPFV
mushipk2_np_	TTDLEGSDML	VEKADRREFI	DLLKKMLTID	ADKRVTPIET	LNHPFV
wormf20b6_q1	GFESDPVEHL	CDRIDRQEFV	DVLKKMLVLN	PDFRITPAEG	LESKFV
humhipk4.kd.	RLTFPDREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV
monkeyhipk4_	RLTFPDREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV
mushipk4.kd.	RLSFDPREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV
rathipk4_xp_	RLSFDPREAL	AEHADLKSMV	ELIKRMLTWE	SHERISPSAA	LRHPFV
yeastyak1_np	SIQNSQELID	QEMQNRECLI	HFLGGVLNLN	PLERWTPQQA	MLHPFI
dmcg17090_q9	HIIAKGNSYR	VPRHEKKEHQ	QLSPVKKRVK	ESSPPHQQRY	QRAAHV

**B**



## FIGURE 7

**A**

CLUSTAL W multiple sequence alignment results

MSF: 340 Type: P Check: 1950 ..

```

Name: musdyrk1a_np_031916.kd.pep oo   Len: 340 Check: 8276 Weight: 2.2
Name: ratdyrk1a_np_036923.kd.pep oo   Len: 340 Check: 8276 Weight: 2.2
Name: humdyrk1a_np_001387.kd.pep oo   Len: 340 Check: 8161 Weight: 2.2
Name: humdyrk1b_np_004705.kd.pep oo   Len: 340 Check: 7992 Weight: 3.5
Name: musdyrk1b_np_034222.kd.pep oo   Len: 340 Check: 6091 Weight: 2.6
Name: dmmnb_aaf48776.kd.pep oo   Len: 340 Check: 7580 Weight: 5.3
Name: wormt04c10_q22155.kd.pep oo   Len: 340 Check: 9628 Weight: 8.0
Name: dmsmi35a_q9v3d5.kd.pep oo   Len: 340 Check: 6217 Weight: 8.4
Name: humdyrk4_dyr4_human.kd.pep oo   Len: 340 Check: 1420 Weight: 8.0
Name: humdyrk2_np_006473.kd.pep oo   Len: 340 Check: 8233 Weight: 6.6
Name: humdyrk3_np_003573.kd.pep oo   Len: 340 Check: 8166 Weight: 7.5
Name: wormf49e11_q20604.kd.pep oo   Len: 340 Check: 7542 Weight: 7.5
Name: kab7_schpo.kd.pep oo   Len: 340 Check: 9798 Weight: 11.1
Name: pom1_schpo.kd.pep oo   Len: 340 Check: 8379 Weight: 9.8
Name: humhipk4.kd.pep oo   Len: 340 Check: 8285 Weight: 3.5
Name: monkeyhipk4_ab074449.kd.fas.pe oo   Len: 340 Check: 8293 Weight: 3.5
Name: mushipk4.kd.pep oo   Len: 340 Check: 9829 Weight: 3.5
Name: rathipk4_xp_218355.kd.pep oo   Len: 340 Check: 9784 Weight: 3.5

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//

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1
musdyrk1a_np YEIDSLIGKG SFGQVVKAYD RVEQEWVAIK IIKNKKAF LN QAQIEVRLLE
ratdyrk1a_np YEIDSLIGKG SFGQVVKAYD RVEQEWVAIK IIKNKKAF LN QAQIEVRLLE
humdyrk1a_np YEIDSLIGKG SFGQVVKAYD RVEQEWVAIK IIKNKKAF LN QAQIEVRLLE
humdyrk1b_np YEIDSLIGKG SFGQVVKAYD HQTQELVAIK IIKNKKAF LN QAQIELRLLE
musdyrk1b_np YEIDSLIGKG SFGQVVKAYD HQTQELVAIK IIKNKKAF LN QAQIELRLLE
dmmnb_aaf487 YEIDSLIGKG SFGQVVKAYD HEEQCHVAIK IIKNKKPFLN QAQIEVKLLE
wormt04c10_q ILSDTPVGKG SFGQVTKAYD TLNKEEVAIK IIKNKKTF FD QAQIEIHLLE
dmsmi35a_q9v YEILEVIGKG SFGQVIRALD HKTNTNTHVAIK IIRNKKRFLN QAVVELNILD
humdyrk4_dyr YEVLKTVIGKG SFGQVAKCLD HKNNELVALK IIRNKKRFHQ QALMELKILE
humdyrk2_np_ YEVLKTVIGKG SFGQVVKAYD HKVHQHVALK MVRNEKRFHR QAAEEIRILE
humdyrk3_np_ YEVLKIIGKG SFGQVARVYD HKLRQYVALK MVRNEKRFHR QAAEEIRILE
wormf49e11_q YEVLKTVIGKG SFGQVIKAFD HKYQQYVALK LVRNEKRFHR QADEEIRILD
kab7_schpo.k YEIIDTVGKG SFGQVLKCID HKRGQVVAIK VIKNRQKFHG QTLVEVGILK
pom1_schpo.k YEIVDFLGKG SFGQVLR CID YETGKLVALK IIRNKKRFHM QALVETKILQ
humhipk4.kd. YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
monkeyhipk4_ YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRNR IIKNELKLLH
mushipk4.kd. YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR
rathipk4_xp_ YDIIEVLGKG TFGEVAKGWR RSTGEMVAIK ILKNDAYRSR IIKNELKLLR
50

```

51

100

musdyrk1a_np	LMNKHDTEMK	YYIVHLKRHF	MFRNHLCLVF	EMLSYNLYDL	LRNTNFRGVS
ratdyrk1a_np	LMNKHDTEMK	YYIVHLKRHF	MFRNHLCLVF	EMLSYNLYDL	LRNTNFRGVS
humdyrk1a_np	LMNKHDTEMK	YYIVHLKRHF	MFRNHLCLVF	EMLSYNLYDL	LRNTNFRGVS
humdyrk1b_np	LMNQHDTEMK	YYIVHLKRHF	MFRNHLCLVF	ELLSYNLYDL	LRNTHFRGVS
musdyrk1b_np	LMNQHDTEMK	YYIVHLKRHF	MFRNHLCLVF	ELLSYNLYDL	LRNTHFRGVS
dmmnb_aaf487	MMNRADAENK	YYIVKLKRHF	MWRNHLCLVF	ELLSYNLYDL	LRNTNFRGVS
wormt04c10_q	LTNAHDKDNK	YNIVTLKGHF	VHRAHLCLVF	ELLSYNLYDL	LKNTSFRGVS
dmsmi35a_q9v	ELREKADAGS	HNVIHMLDYT	YFRKHLCLTF	ELMSLNLYEL	IKKNNYNGFS
humdyrk4_dyr	ALRKDKDNT	YNVVHMKDFF	YFRNHFCITF	ELLGINLYEL	MKNNNFQGF
humdyrk2_np	HLRKQDKDNT	MNVIHMLENF	TFRNHICMTF	ELLSMNLyel	IKKNKFQGF
humdyrk3_np	HLKKQDKTGS	MNVIHMLESF	TFRNHVCMAT	ELLSIDLYEL	IKKNKFQGF
wormf49e11_q	HLRRQSDSGT	HNIIHMLDYF	NFRNHKCITF	ELLSINLYEL	IKRNKFQGF
kab7_schpo.k	RLCEADPADK	NNVIRYLSHF	DFRGHLCIVT	ELLSGNLFDV	IRENNYKGLP
pom1_schpo.k	KIREWDPLDE	YCMVQYTDHF	YFRDHLCVAT	ELLGKNLYEL	IKSNGFKGLP
humhipk4.kd.	CMRGLDPE.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP
monkeyhipk4	CMRGLDPE.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP
mushipk4.kd.	CVRGLDPD.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP
rathipk4_xp	CVRGLDPD.E	AHVIRFLEFF	HDALKFYLVF	ELLEQNLFEF	QKENNFAPLP

101

150

musdyrk1a_np	LNLTRKFAQQ	MCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
ratdyrk1a_np	LNLTRKFAQQ	MCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
humdyrk1a_np	LNLTRKFAQQ	MCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
humdyrk1b_np	LNLTRKLAQQ	LCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
musdyrk1b_np	LNLTRKLAQQ	LCTALLFLAT	PELSIIHCDL	KPENILLCNP	KRS..AIKIV
dmmnb_aaf487	LNLTRKFAQQ	LCTALLFLST	PELNIIHCDL	KPENILLCNP	KRS..AIKIV
wormt04c10_q	LNLARKFAQQ	LGKTLLFLSS	PELSIIHCDL	KPENVLLVNA	KRS..QIRVI
dmsmi35a_q9v	MSLIRRFCNS	IVKCLRLLY.	.KENIIHCDL	KPENILLKQR	GSS..SIKVI
humdyrk4_dyr	LSIVRRFTLS	VLKCLQMLS.	.VEKIIHCDL	KPENIVLYQK	GQA..SVKVI
humdyrk2_np	LPLVRKFAHS	ILQCLDALH.	.KNRIIHCDL	KPENILLKQQ	GRS..GIKVI
humdyrk3_np	VQLVRKFAQS	ILQSLDALH.	.KNKIIHCDL	KPENILLKHH	GRS..STKVI
wormf49e11_q	LMLVRKFAYS	MLLCLDLLQ.	.KNRLIHCDL	KPENVLLKQQ	GRS..GIKVI
kab7_schpo.k	LIVVKSFALQ	GLQALRLLO.	.GQNIIHCDL	KPENLLLSHP	LKA..RIKLI
pom1_schpo.k	IVVKSITRQ	LIQCLTLLN.	.EKHVIHCDL	KPENILLCHP	FKS..QVKVI
humhipk4.kd.	ARHIRTVTLO	VLTAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI
monkeyhipk4	ARHIRTVTLO	VLRAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI
mushipk4.kd.	ARHIRTVTLO	VLRAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI
rathipk4_xp	ARHIRTVTLO	VLRAARLK.	.ELAIIHADL	KPENIMLVDQ	TRCPFRVKVI

	151				200
musdyrk1a_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE
ratdyrk1a_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE
humdyrk1a_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGMPYDLAID	MWSLGCILVE
humdyrk1b_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGTPYDLAID	MWSLGCILVE
musdyrk1b_np	DFGSSCQLGQ	R...IYQYIQ	SRFYRSPEVL	LGTPYDLAID	MWSLGCILVE
dmmnb_aaf487	DFGSSCQLGQ	R...IYHYIQ	SRFYRSPEVL	LGIQYDLAID	MWSLGCILVE
wormt04c10_q	DFGSSCQTGH	R...IYQYIQ	SRFYRSPEVL	LGIAYDTKID	MWSLGCILVE
dmsmi35a_q9v	DFGSSCYVDR	K...IYTYIQ	SRFYRSPEVI	LGLQYGTALD	MWSLGCILAE
humdyrk4_dyr	DFGSSCYEHQ	K...VYTYIQ	SRFYRSPEVI	LGHYPYDVAID	MWSLGCITAE
humdyrk2_np	DFGSSCYEHQ	R...VYTYIQ	SRFYRAPEVI	LGARYGMPID	MWSLGCILAE
humdyrk3_np	DFGSSCFEYQ	K...LYTYIQ	SRFYRAPEII	LGSRYSTPID	IWSFRCILAE
wormf49e11_q	DFGSSCFDDQ	R...IYTYIQ	SRFYRAPEVI	LGTKYGMPID	MWSLGCILAE
kab7_schpo.k	DFGSSCFYNE	K...VYTYLQ	SRFYRAPEII	LGLEYGKEID	IWSFGCILAE
pom1_schpo.k	DFGSSCFEGE	C...VYTYIQ	SRFYRSPEVI	LGMGYGTPID	VWSLGCIIAE
humhipk4.kd.	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE
monkeyhipk4	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE
mushipk4.kd.	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE
rathipk4_xp	DFGSASIFSE	VRYVKEPYIQ	SRFYRAPEIL	LGLPFCEKVD	VWSLGCVMAE

	201				250
musdyrk1a_np	MHTGEPLFSG	ANEVDQMNKI	VEVLGIPPAH	ILDQAPKARK	FFEKLDPDGTW
ratdyrk1a_np	MHTGEPLFSG	ANEVDQMNKI	VEVLGIPPAH	ILDQAPKARK	FFEKLDPDGTW
humdyrk1a_np	MHTGEPLFSG	ANEVDQMNKI	VEVLGIPPAH	ILDQAPKARK	FFEKLDPDGTW
humdyrk1b_np	MHTGEPLFSG	SNEVDQMNRI	VEVLGIPPAH	MLDQAPKARK	YFERLPGGGW
musdyrk1b_np	MHTGEPLFSG	SNEVDQMSRI	VEVLGIPPAH	MLEQAPKARK	YFERLPGGGW
dmmnb_aaf487	MHTGEPLFSG	CNEVDQMNKI	VEVLGMPPKY	LLDQAHKTRK	FFDKIVADGS
wormt04c10_q	MHTGEPLFAG	SSEVDQMMKI	VEVLGMPPKE	MLDIGPKTHK	YFDKTEDGIY
dmsmi35a_q9v	LYTGFPLFPG	ENEVEQLACI	MEVLGLPPKV	LISVARRRRL	FFDSRDAPRC
humdyrk4_dyr	LYTGYPLFPG	ENEVEQLACI	MEVLGLPPAG	FIQTASRRQT	FFDSKGFPKN
humdyrk2_np	LLTGYPLLP	EDEGDQLACM	IELLGMPSQK	LLDASKRAKN	FVSSKGYPRY
humdyrk3_np	LLTGQPLFPG	EDEGDQLACM	MELLGMPPPK	LLEQSKRAKY	FINSKGIPRY
wormf49e11_q	LLTGYPLLP	EDENDQLALI	IELLGMPPPK	SLETAKRART	FITSKGYPRY
kab7_schpo.k	LFTGVPLFPG	GNETEQLGYI	MEVLGPPMA	LIRNSTRSKA	YFDSEKPHP
pom1_schpo.k	MYTGFPLFPG	ENEQEQLACI	MEIFGPPDHS	LIDKCSRKKV	FFDSSGKPRP
humhipk4.kd.	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAACKAHH	FFKRNPHPDA
monkeyhipk4	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAACKAHH	FFKRNPHPDA
mushipk4.kd.	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAACKAHH	FFKRNPHPDA
rathipk4_xp	LHLGWPLYPG	NNEYDQVRYI	CETQGLPKPH	LLHAACKAHH	FFKRNPHPDA

	251				300
musdyrk1a_np	SLKKT.....	.....K	DGKREYKPPG	TRKLHNILGV	ETGGPGGRRRA
ratdyrk1a_np	SLKKT.....	.....K	DGKREYKPPG	TRKLHNILGV	ETGGPGGRRRA
humdyrk1a_np	NLKKT.....	.....K	DGKREYKPPG	TRKLHNILGV	ETGGPGGRRRA
humdyrk1b_np	TLRRT.....	.....K	ELRKDYQGP	TRRLQEV LGV	QTGGPGGRRRA
musdyrk1b_np	TLRRT.....	.....K	ELR.....	.....	.....
dmmnb_aaf487	YVLKK.....	.....N	QNGRKYKPPG	SRKLHDILGV	ETGGPGGRRRL
wormt04c10_q	YCKKTR....	.....D	GYRHTYKAPG	ARKLHEILGV	TSGGPGGRRRL
dmsmi35a_q9v	ITNT.....	.....	.....	.....KG	RKRSPGSKS.
humdyrk4_dyr	ITNN.....	.....	.....	.....RG	KKRYPDSKD.
humdyrk2_np	CTVTT.....	.....	....LSDGSV	VLNGGRSRRG	KLRGPPEFRE
humdyrk3_np	CSVTT.....	.....	....QADGRV	VLVGGRSRRG	KKRGPPGSKD
wormf49ell_q	CTATS.....	.....	....MPDGSV	VLGARSKR	KMRGPPASRS
kab7_schpo.k	ITDS.....	.....	.....	.....	HNRLLPSTR
pom1_schpo.k	FVSS.....	.....	.....	.....	KGVSRRPFSK
humhipk4.kd.	ANPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	SVASRLTFPD
monkeyhipk4	ANPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	SVASRLTFPD
mushipk4.kd.	TNPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	GAVSRLSFPD
rathipk4_xp	TNPWQLKSSA	DYLAETKVRP	LERRKYMLKS	LDQIETVNGG	GAVNRLSFPD

	301				340
musdyrk1a_np	GESGHTVADY	LKFKDLILRM	LDYDPKTRIQ	PYYALQHSFF	
ratdyrk1a_np	GESGHTVADY	LKFKDLILRM	LDYDPKTRIQ	PYYALQHSFF	
humdyrk1a_np	GESGHTVADY	LKFKDLILRM	LDYDPKTRIQ	PYYALQHSFF	
humdyrk1b_np	GEPGHSPADY	LRFQDLVLRM	LEYEPAARIS	PLGALQHGF	
musdyrk1b_np	.....	...KDLVLRM	LEYEPAARIS	PLGALQHGF	
dmmnb_aaf487	DEPGHSVSDY	LKFKDLILRM	LDYDPKTRVT	PYYALQHNF	
wormt04c10_q	GEPGHSVEDY	SKFKDLIKRM	LQFDPKQRIS	PYYVVRHPFL	
dmsmi35a_q9v	.LAHILHCQD	RYFIDFLQRC	LEWDPAERMT	PDEAAHHEFL	
humdyrk4_dyr	.LTMVLKTYD	TSFLDFLRRC	LVWEPRLMT	PDQALKHAWI	
humdyrk2_np	WGNALKGCD	PLFLDFLKQC	LEWDPAVRMT	PGQALRHPWL	
humdyrk3_np	WGTALKGCD	YLFIEFLKRC	LHWDPSARLT	PAQALRHPWI	
wormf49ell_q	WSTALKNMGD	ELFVDFLRRC	LDWDPETRMT	PAQALKHKWL	
kab7_schpo.k	TFSQLLNTKQ	ASFLDFLSKC	LKWDPKDRIT	VDSALQHEFI	
pom1_schpo.k	SLHQVLQCKD	VSFLSFISDC	LKWDPPERMT	PQQAAQHDFL	
humhipk4.kd.	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	
monkeyhipk4	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	
mushipk4.kd.	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	
rathipk4_xp	REALAEHADL	KSMVELIKRM	LTWESHERIS	PSAALRHPFV	

**B**

